

GenCore version 4.5
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Om protein - protein search, using sw model

Run on: January 30, 2002, 11:49:01 ; Search time 18.17 Seconds
(without alignments)
26.232 Million cell updates/sec

Title: US-09-432-546-4

Perfect score: 99
Sequence: 1 RRRPWWPKWPLI 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3666427 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	62.6	144	1 INDC_BOVIN	P33046 bos taurus
2	52	52.5	1112	1 CN3B_HUMAN	Q13370 homo sapien
3	51.5	52.5	1112	1 ADRO_BOVIN	P08165 bos taurus
4	51	51.5	1113	1 VGL2_CVH22	P15423 human corona
5	50.5	51.0	278	1 RCEL_RHOGE	P51760 rhodococcus
6	50.5	51.0	494	1 ADRO RAT	P56522 rat
7	49.5	50.0	253	1 Y9K4 MYCUT	P71564 mycobacterium
8	49.5	50.0	491	1 ADRO_HUMAN	P22570 homo sapien
9	48.5	49.0	212	1 PFL1_PIG	P51524 sus scrofa
10	48.5	49.0	228	1 PFL2_PIG	P51525 sus scrofa
11	48	48.5	990	1 ENV_OINVY	P16899 ovine lentil
12	47	47.5	942	1 ENV_CAEVG	P31627 caprine art
13	47	47.5	966	1 ENV_CAEVC	P31626 caprine art
14	47	47.5	982	1 ENV_VILV	P03379 visna lentil
15	47	47.5	983	1 ENV_VILVK	P35954 visna lentil
16	47	47.5	989	1 ENV_VILVI	P23422 visna lentil
17	47	47.5	991	1 ENV_VILV2	P23423 visna lentil
18	46	46.5	533	1 UBB_FSEAE	Q9hub8 pseudomonas
19	46	46.5	572	1 GAG_IPHA	P04023 hamster int
20	45.5	46.0	1660	1 FBHU_ECOLI	P05972 escherichia
21	45	45.5	115	1 NUFM_BOVIN	P23935 bovis taurinus
22	45.5	45.5	115	1 NUFR RAT	Q83362 rattus norvegicus
23	45	45.5	214	1 AVEN_AVEVA	P27919 avena sativa
24	45	45.5	534	1 APG_ARATH	P4602 arabiadopsis
25	45.5	45.5	722	1 ACM1_DROME	P16395 drosophila
26	44	44.4	115	1 NUFM_HUMAN	Q16718 homo sapiens
27	44	44.4	407	1 FUCO_CAEEL	P49113 caenorhabditis
28	44	44.4	485	1 AERS_AERY	Q06306 aeromonas
29	44	44.4	488	1 AERA_AERSO	Q06304 aeromonas
30	44	44.4	489	1 AERL_AERSA	Q08676 aeromonas
31	44	44.4	492	1 AER3_AERY	Q06303 aeromonas
32	44	44.4	492	1 AERA4_AERY	Q06303 aeromonas
33	44	44.4	492	1 AERL_AERTR	P09166 aeromonas

RESULT 1

ID INDC_BOVIN STANDARD; PRT; 144 AA.

INDC_BOVIN P33046; 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE INDOPLICIDIN PRECURSOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE-92392368; PubMed-1520337;
RA del Sal G., Storisi P., Schneider C., Romeo D., Zanetti M.; RT "CDNA cloning of the neutrophil bactericidal peptide indolicidin.";
RL Biochem. Biophys. Res. Commun. 187:467-472(1992).
RN [2]
RP SEQUENCE OF 131-143.
RC TISSUE=Neutrophils;
RX MEDLINE-92165771; PubMed-1537821;
RA Seisted M.E., Novotny M.J., Morris W.L., Tang Y.-Q., Smith W., Cullo J.S.; RT "Indolicidin," a novel bactericidal tridecapeptide amide from neutrophils"; J. Biol. Chem. 267:4292-4295(1992).
RL - FUNCTION: POTENT MICROBIAL ACTIVITY, ACTIVE AGAINST STAPHYLOCOCCUS AUREUS AND ESCHERICHIA COLI.
CC -- TISSUE SPECIFICITY: LARGE GRANULES OF NEUTROPHILS.
CC -! PTM: ELASTASE MIGHT BE RESPONSIBLE FOR ITS MATURATION.
CC -! SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
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CC
EMBL; X67340; CPA47755.1; -
DR PIR; JC1222; JC1222.
DR PIR; A42387; A42387.
DR InterPro; IPR001894; Cathelicidin.
DR Pfam; PF00666; Cathelicidins; 1.
DR PRODOM; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHHELICIDINS_2; 1.
KW Antibiotic; Amidation; Signal.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 130
FT PEPTIDE 131 143 INDOPLICIDIN.
FT MOD_RES 30 30 PYRROLIDONE CARBOXYLIC ACID (BY

Query Match 85 96
Best Local Similarity 75.0%; Pred. No. 0.088; Score 62; DB 1; Length 144;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Ov 2 RWPWPKW 9
Db 135 KWPWWPWR 142

RESULT 2
CN3B_HUMAN STANDARD PRT; 112 AA.
ID CN3B_HUMAN
AC Q13370; 000639; Q14408;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CGMP-INHIBITED 3',5'-CYCLIC PHOSPHODIESTERASE B (EC 3.1.4.17) (CYCLIC GMP-INHIBITED PHOSPHODIESTERASE B) (CGIPDE1) (CGIP1).
GN PDE3B
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TAXID=9606;
RN [1]
RP SEQUENCE FROM N.A.
Tissue_Fat; MEDLINE=97038690; PubMed=88084271;
RA MIKI T., Taira M., Hockman S., Shimada F., Lieman J., Napolitano M., Ward D., Taira M., Matino H., Manganiello V.C.;
RT "Characterization of the cDNA and gene encoding human PDE3B, the cGMP isoform of the human cyclic GMP-inhibited cyclic nucleotide phosphodiesterase family.",
RL Genomics 36:476-485(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=97039687; PubMed=8821398;
RA Leibert R.W., Winterbach A., Selpel B., Zabel B.U.;
RT "Molecular cloning and chromosomal assignment of the human homologue of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A) -- a gene involved in fat metabolism located at 11p15.1.",
RT Genomics 37:211-218(1996).
RN [1]
RP FUNCTION: MAY PLAY A ROLE IN FAT METABOLISM.
CC -!- CATALYTIC ACTIVITY: GUANOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O = GUANOSINE 5'-PHOSPHATE.
CC -!- ENZYME REGULATION: INHIBITED BY CGMP.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).
CC -!- TISSUE SPECIFICITY: ABUNDANT IN ADIPOSE TISSUES.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.
CC -----
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Query Match 52.5%; Score 52; DB 1; Length 112;
Best Local Similarity 62.5%; Pred. No. 9.6; Score 52; DB 1; Length 144;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Ov 3 WPWPKW 10
Db 169 WQWNSWPW 176

RESULT 3
ADRO_BOVIN STANDARD PRT; 492 AA.
ID ADRO_BOVIN
AC P08165;
DT 01-AUG-1998 (Rel. 08, Created)
DT 20-AUG-2001 (Rel. 36, Last sequence update)
DE NADPH/ADRENODOXIN OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR (EC 1.18.1.2) (ADRENODOXIN REDUCTASE) (AR) (FERREDOXIN-NADP(+))
DE REDUCTASE[1]
RN PDXR OR ADXR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovine; Bos.
OC NCBI_TAXID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=9417140; PubMed=8130767;
RA Takata Y., Sagara Y., Kono A., Sekimizu K., Horiochi T.;
RT "Gene structure of bovine adrenodoxin reductase.";
RL Biol. Pharm. Bull. 16:1200-1206(1993).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=88198050; PubMed=348886;
RA Sagara Y., Takata Y., Minata T., Hara T., Horiochi T.;
RT "cloning and sequence analysis of adrenodoxin reductase cDNA from bovine adrenal cortex.";
J. Biochem. 102:1333-1336(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87270696; PubMed=3038094;
RA Nonaka Y., Murakami H., Yabasaki Y., Kuramitsu S., Kagamiyama H., Yamano T., Okamoto M.;
RT "Molecular cloning and sequence analysis of full-length cDNA for mRNA of adrenodoxin oxidoreductase from bovine adrenal cortex.";
RL Biochem. Biophys. Res. Commun. 145:1239-1247(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE-Adrenal cortex;
RX MEDLINE=89170752; PubMed=2924777;
RA Hanukoglu I., Gutfinger T.;

Matches	7;	Conservative	0;	Mismatches	3;	Indels	1;	Gaps	1;
QY	1	RRWPWPPW-KW	10						
ID	VGL2_CVH22								
AC	P15423;								
DB	4 RCWPPWPSWW	14							
RESULT	4								
VGL2_CVH22									
STANDARD;									
PRT;									
1173 AA.									
DT	01-APR-1990	(Rel. 14, Created)							
DT	01-APR-1990	(Rel. 14, Last sequence update)							
DT	15-JUL-1999	(Rel. 38, Last annotation update)							
DE	E2 GLYCOPROTEIN PRECURSOR (Spike glycoprotein)	(Peplomer protein).							
GN	S								
OS	Human coronavirus (strain 229E)								
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;								
OX	Coronaviridae; Coronavirous.								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=90264837; PubMed=2345367;								
RA	Raab T.; Schelle-Prinz B.; Siddell S.G.;								
RT	"Nucleotide sequence of the gene encoding the spike glycoprotein of human coronavirus HCV 229E."								
RL	J. Gen. Virol. 71:1065-1073(1990).								
CC	-!- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION								
CC	AND IN SYNCYTIA FORMATION.								
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.								
CC	-----								
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DR	EMBL; X16816; CAA34723.1; .								
DR	PIR: A34766; V01HC.								
DR	InterPro; IPR002551; Corona_S1.								
DR	ProDom; PF01600; Corona_S2.								
DR	Pfam; PF01601; Corona_S2; 1.								
KW	Glycoprotein; Envelope protein; transmembrane; Signal.								
FT	SIGNAL	1	15						
FT	CHAIN	16	1173						
FT	DOMAIN	16	1173						
FT	TRANSMEM	1116	1135						
FT	DOMAIN	1136	1173						
FT	CARBOHYD	1136	1157						
FT	CARBOHYD	23	23						
FT	CARBOHYD	62	62						
FT	CARBOHYD	98	98						
FT	CARBOHYD	147	147						
FT	CARBOHYD	171	171						
FT	CARBOHYD	176	176						
FT	CARBOHYD	220	220						
FT	CARBOHYD	243	243						
FT	CARBOHYD	326	326						
FT	CARBOHYD	332	333						
FT	CARBOHYD	440	440						
FT	CARBOHYD	464	464						
FT	CARBOHYD	518	518						
FT	CARBOHYD	538	538						
FT	CARBOHYD	542	542						
FT	CARBOHYD	568	568						
FT	CARBOHYD	581	581						
FT	CARBOHYD	587	587						
FT	CARBOHYD	663	663						
FT	CARBOHYD	671	671						

Thu Jan 31 11:07:40 2002

FT	CARBONYD	930	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBONYD	1015	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBONYD	1020	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBONYD	1037	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBONYD	1049	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBONYD	1061	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBONYD	1066	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBONYD	1076	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBONYD	1082	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBONYD	1096	N-LINKED (GLCNAC. . .)	(POTENTIAL)
SO	SEQUENCE	1173	AA;	128639 MW;
				B9CA941A796B3BD CRC64;

EMBL: U30310; AAA73927.1; -.
 DR EMBL; U5198; RAB41576.1; -.
 DR HSSP; P02954; 2SCR.
 DR Interpo; IPR000484; Photo_RC.
 DR Pfam; PF00124; photorc_1.
 DR PRINTS; PRO0256; REACTNCNTR.
 DR PRODOM; PD000551; Photo_RC; 1.
 DR PROSITE; PS00244; REACTION_CENTER; 1.
 DR Transmembrane; Electron_transport; Photosynthesis; Reaction_center;
 KW Iron; Magnesium; 0
 FT INIT_MET 0 BY SIMILARITY.
 FT TRANSMEM 32 POTENTIAL.
 FT TRANSMEM 84 112 POTENTIAL.
 FT TRANSMEM 115 140 POTENTIAL.
 FT TRANSMEM 170 199 POTENTIAL.
 FT TRANSMEM 251 251 POTENTIAL.
 FT TRANSMEM 173 173 MAGNESIUM (BACTERIOCHLOROPHYLL B) (BY
 METAL
 FT (MAGSUSP)

	Matches	5;	Conservat.
OY	2	RWPWMPW	8
Db	1113	KWPWMWV	1119

SQ SEQUENCE 278 AA; 31210 MW, 0.000000

AC P3176U
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE REACTION CENTER PROTEIN L CHAIN (PHOTOSYNTHETIC REACTION CENTER L
DE REACTION CENTER PROTEIN L CHAIN (PHOTOSYNTHETIC REACTION CENTER L

RESULT - 6

OC
OC
Rubrivivax.
NCBI_TAXID=28068;
OX

RX
RA
RT
MEDLINE-#4132001; Kuboura S., Ohwara S., Shimada K.; NADASIMA K.V.P., Matsubara K., Ohwara S., Shimada K.; "Primary structure and transcription of genes encoding B870 and primary antibody reaction center apoproteins from Rubrivivax

Rattus norvegicus (Rat); Chordata; Craniata; Vertebrata; Euteleostomi; OS OC Eukaryota; Metazoa; Sciurognathi; Muridae; Murinae; Rattus

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S1;

RP
SEQUENCE FROM NCBI;
STRAIN=MISTER; TISSUE=Adrenal gland;
MENID LINE=99454627; PubMed=10525147;

RT construction, characterization and comparison with
RT deletion strain." *J Appl Polym Sci* 60: 352-379-385 (1996).

RL Biochim. Biophys. Acta 1434: 284-295 (1991).
CC -!- FUNCTION: SERVES AS THE FIRST ELECTRON TRANSFER PROTEIN IN ALL THESE
-!- SYSTEMS INCLUDING CHOLESTEROL SIDE CHAIN

-1- SUBUNIT: REACTION CENTER IS COMPOSED OF FOUR BACTERIOPHOTOPHYTINS. TWO BACTERIOPHEOPHYTINS, TWO UBIQUINONES, ONE IRON, AND THREE AMINO ACIDS DESIGNATED L, M, AND H.

CC
CC
HYDROXYLATION IN THE KIDNEY,
LIVER.
COMPARATIVE ACTIVITY: REDUCED ADRENODOXIN + NADP(+) = OXIDIZED

PSBD FAMILY.

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 EMBL; D63761; BAA23759.1; -.
 DR InterPro; IPR000755; Admrx_reductse.
 DR PRINTS; PR00419; ADXRDRASE.
 KW Electron transport, OXIDOREDUCTASE; Flavoprotein; NADP; FAD;
 KW Mitochondrion; TRANSIT peptide.
 FT CHAIN 1 34 MITOCHONDRIUM.
 FT 35 494 AA; 54362 MW; SF07837DFA9525D CRC64;
 SQ SEQUENCE 494 AA; 54362 MW; SF07837DFA9525D CRC64;

Query Match 51.0%; Score 50.5; DB 1; Length 494;
 Best Local Similarity 58.3%; Pred. No. 7.2%;
 Matches 7; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 1 RRPWWWWK-WP 11
 | | | | |
 Db 4 RCWRWWWSAWP 15

RESULT 7
 Y445_MYCTU STANDARD; PRT; 253 AA.
 ID Y445_MYCTU AC PT1564;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DT PUTATIVE_OXIDOREDUCTASE RV0945 (EC 1.1.1.1).
 GN RV0945 OR MT0971 OR MICY10D7.29C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RP STRAIN="H72RV;"
 RX MEDLINE=9229587; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglemeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J.J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Ruttritt S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544 (1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBry R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam A., Ermlaeva M.D., Silzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SWISS-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.

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DR EMBL; Z79700; CAB02005.1; -.
 DR EMBL; AE006982; AAK45219.1; -.
 DR TIGR; MT0971; -.
 DR Tuberculist; RV0945; -.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PRO0106; adh_short; 1.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KW Hypothetical protein; Oxidoreductase; Complete proteome.
 FT ACT_SITE 159 159 BY SIMILARITY.
 SQ SEQUENCE 253 AA; 27138 MW; BAD937208842DA12 CRC64;

Query Match 50.0%; Score 49.5; DB 1; Length 253;
 Best Local Similarity 70.0%; Pred. No. 5.3%;
 Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 QY 4 PWPPWKPLI 13
 Db 230 PWPPWPA-PLV 238

RESULT 8
 ADRO_HUMAN STANDARD; PRT; 491 AA.
 ID ADRO_HUMAN AC P22570; Q13716;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE NADPH:ADRENODOXIN_OXIDOREDUCTASE; MITOCHONDRIAL PRECURSOR
 DE (EC 1.8.1.2) (ADRENODOXIN REDUCTASE) (AR) (FERRREDOXIN-NADP(+))
 DE REDUCTASE.
 GN FDXR OR ADXR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Primates; Catarrhini; Hominoidea; Homo.
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89017146; PubMed=2845396;
 RA Solish S.B., Picado-Leonard J., Morel Y., Kuhn R.W., Mohandas T.K.,
 RA Hanukoglu I., Miller W.L.;
 RT Human adrenodoxin reductase: two mRNAs encoded by a single gene on
 RT chromosome 17cen->q25 are expressed in steroidogenic tissues.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7104-7108(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=910628; PubMed=2236061;
 RA Lin D., Shi Y., Miller W.L.;
 RT "Cloning and sequence of the human adrenodoxin reductase gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8316-8320(1990).
 CC -!- FUNCTION: SERVES AS THE FIRST ELECTRON TRANSFER PROTEIN IN ALL THE
 CC MITOCHONDRIAL P450 SYSTEMS INCLUDING CHOLESTEROL SIDE CHAIN
 CC CLEAVAGE IN ALL STEROIDOGENIC TISSUES, STEROID 11-BETA
 CC HYDROXYLATION IN THE ADRENAL CORTEX, 25-OH-VITAMIN D3, 24
 CC HYDROXYLATION IN THE KIDNEY, AND STEROL C-27 HYDROXYLATION IN THE
 CC LIVER.
 CC -!- CATALYTIC ACTIVITY: REDUCED ADRENODOXIN + NADP(+) = OXIDIZED
 CC ADRENODOXIN + NADPH.
 CC -!- COFACTOR: FAD.
 CC -!- PATHWAY: CHOLESTEROL SIDE-CHAIN-CLEAVAGE SYSTEM.
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A SHORT FORM (SHOWN HERE) AND A
 CC LONG FORM: ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM
 CC REPRESENTS 10-20% OF ALL ADRENODOXIN REDUCTASE mRNA. AND SEEMS TO
 CC BE INACTIVE.

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CC DR EMBL; J03826; AAB59478.1; -.
 CC DR EMBL; J03826; AAB59497.1; -.
 CC DR EMBL; M58509; AA51668.1; -.
 CC DR EMBL; M58509; AA51669.1; JOINED.
 CC DR EMBL; M58509; AA51669.1; -.
 CC DR PIR; A36482; A36482.
 CC DR PIR; A40487; A40487.
 CC DR MM; 103270; -;
 DR InterPro; IPR00759; Adrndx_redactse.
 DR PRIMUS; PR00419; ADXRDASE.
 KW Electron transport; Oxidoreductase; Flavoprotein; NADP; FAD;
 KW Mitochondrion; Transf peptide; Alternative splicing; Polymorphism.
 FT MITOCHONDRION.
 FT CHAIN TRANSIT 1 33 491 NADPH:ADENOXIN OXIDOREDUCTASE.
 FT VARSPLIC 203 203 E -> EA(LICQ) (IN LONG ISFORM).
 FT VARIANT 123 123 0 -> R.
 FT SEQUENCE 491 AA; 53808 MW; /FTID=VAR_004624;
 SQ 85865BA2276D2B2 CRC64;

Query Match 50.0%; Score 49.5; DB 1; Length 491;
 Best Local Similarity 58.3%; Pred. No. 9.6;
 Matches 7; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 1 RRPWPKWPKWPK 11
 Db 4 RCWRNGWSAMP 15

RESULT 9
 PEI1_PIG STANDARD; PRT; 212 AA.
 ID PEI1_PIG
 AC PS1524;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PROPHENIN-1 PRECURSOR (PF-1) (C6) (FRAGMENT).
 OS Sus scrofa (Pig).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC NCBL_TaxID=9823;
 OX [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=95042752; PubMed=7276250;
 RA Strukelj B., Pungercar J., Kopitar G., Renko M., Lenarcic B.,
 RA Berbic S., Turk V.;
 RT "Molecular cloning and identification of a novel porcine
 cathelin-like antibacterial peptide precursor.";
 RL Biol. Chem. Hoppe-Seyler 370:507-510(1995).
 RN [2]
 SEQUENCE OF 131-209.
 RP TISSUE=Blood;
 RX MEDLINE=95212385; PubMed=7698355;
 RA Harwig S.S.L., Kokyakov V.N., Swiderek K.M., Aleshina G.M.,
 RA Zhao C., Lehrer R.I.;
 RT "Prophenin-1, an exceptionally proline-rich antimicrobial peptide
 from porcine leukocytes";
 RT FEBS Lett. 362:65-69(1995).
 -1- FUNCTION: EXERTS ANTIMICROBIAL ACTIVITY. IT IS MORE EFFECTIVE
 AGAINST GRAM NEGATIVE BACTERIA THAN GRAM POSITIVE BACTERIA.
 -1- SIMILARITY: BELONGS TO THE CATHHELICIDIN FAMILY.

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CC DR EMBL; X86031; CAA60023.1; -.
 DR InterPro; IPR001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins_1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 DR Antibiotic; Repeat; Amidation.
 KW Non_TER 1 13 POTENTIAL.
 FT SIGNAL <1 13 POTENTIAL.
 PROPEP 14 130 PROPHENIN-1.
 PEPTIDE 131 209 REMOVED IN MATURE FORM (POTENTIAL).
 PROPEP 210 212 PYRROLIDONE CARBOXYLIC ACID (BY
 MOD_RES 14 14 SIMILARITY).
 FT DOMAIN 116 212 PRO-RICH.
 FT DOMAIN 132 201 7 X 10 AA TANDEM REPEATS.
 FT DISULFID 91 108 BY SIMILARITY.
 FT DISULFID 132 141 AMIDATION (G-210 PROVIDE AMIDE GROUP)
 FT MOD_RES 209 209 (POTENTIAL).
 FT DOMAIN 132 141 1.
 FT REPEAT 142 151 2.
 FT REPEAT 152 161 3.
 FT REPEAT 162 171 4.
 FT REPEAT 172 181 5.
 FT REPEAT 182 191 6.
 FT REPEAT 192 201 7.
 FT SEQUENCE 212 AA; 23956 MW; A315414C90DBF423 CRC64;

Query Match 49.0%; Score 49.5; DB 1; Length 212;
 Best Local Similarity 53.8%; Pred. No. 6;
 Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;
 QY 1 RRPWPKWPKWPKL 13
 Db 113 RRPFWN--WPF 122

RESULT 10
 PEI2_PIG STANDARD; PRT; 228 AA.
 ID PEI2_PIG
 AC PS1525;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PROPHENIN-2 PRECURSOR (PF-2) (PR-2) (C12) (PROPHENIN-1 LIKE).
 OS Sus scrofa (Pig).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC NCBL_TaxID=9823;
 OX [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow; PubMed=9226247;
 RX MEDLINE=94035623; PubMed=9226247;
 RA Pungercar J., Strukelj B., Kopitar G., Renko M., Lenarcic B.,
 RA Gubensk F., Turk V.;
 RT "Molecular cloning of a putative homolog of proline/arginine-rich
 antibacterial peptides from porcine bone marrow.";
 RT FEBS Lett. 336:284-288(1993).
 RN [2]
 SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=9610565; PubMed=7198526;
 RA Zhao C., Ganz T., Lehrer R.I.;
 RT "Structures of genes for two cathelin-associated antimicrobial
 peptides: prophenin-2 and PR-39.";
 RT FEBS Lett. 376:130-134(1995).
 -1- FUNCTION: EXERTS ANTIMICROBIAL ACTIVITY. IT IS MORE EFFECTIVE
 AGAINST GRAM NEGATIVE BACTERIA THAN GRAM POSITIVE BACTERIA.
 -1- SIMILARITY: BELONGS TO THE CATHHELICIDIN FAMILY.

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DR EMBL; X75438; CAA53188.1; -.
 DR EMBL; X89202; CAA61488.1; -.
 DR InterPro; IPR001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; I.
 DR ProDom; PD00838; Cathelicidin; 1.
 DR PROSITE; PS00946; CATHELICIDINS; 1; 1.
 DR PROSITE; PS00947; CATHELICIDINS; 2; 1.
 KW Antibiotic; Repeat; Amidation; Signal.
 FT SIGNAL 1 29
 FT PROPER 30 146
 FT PEPTIDE 147 225
 FT PROPEP 226 228
 FT MOD_RES 225 225
 FT DOMAIN 132 228
 FT DOMAIN 148 217
 FT REPEAT 148 157
 FT REPEAT 158 167
 FT REPEAT 168 177
 FT REPEAT 178 187
 FT REPEAT 188 197
 FT REPEAT 198 207
 FT REPEAT 208 217
 FT MOD_RES 30 30
 FT DISULFID 85 95
 FT DISULFID 107 124
 SQ SEQUENCE 228 AA; 25855 MW; 1EA4511FB35CC182 CRC64;

Query Match 49.0%; Score 48.5; DB 1; Length 228;
 Best local Similarity 53.8%; Pred. No. 6 4;
 Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

Qy 1 RRWPPWWPKWPL 13
 ||:||| :||| :|||

Db 129 RREPW--WPRL 138

RESULT 11.
 ENV_OMVNS STANDARD; PRT; 990 AA.

ID ENV_OMVNS
 AC P16899;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE ENV POLYPROTEIN PRECURSOR (COAT POLYPEPTIDE).

GN ENV.
 OS Ovine lentivirus (strain SA-OMV).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TAXID=11664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9023989; PubMed=2158181;
 RA Querat G., Audoly G., Sonigo P., Vigne R.;
 RT "Nucleotide sequence analysis of SA-OMV, a visna-related ovine
 lentivirus, phylogenetic history of lentiviruses.";
 RL virology 175:43-47(1990).

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DR EMBL; M34193; AAA46783.1; -.
 DR EMBL; M31616; ARH6817.1; -.
 DR PIR; G46335; G46335.
 DR HIV; M34193; ENVSOMVWSACG.
 DR InterPro; IPR000328; Env_SP41.
 DR Pfam; PF00317; GP41; 1.
 KW Glycoprotein; Coat protein; Polyprotein; Transmembrane.
 FT PEPTIDE 1 101
 FT CHAIN 102 662
 FT TRANSMEMBANE 842 863
 FT CARBOHYD 141 141
 FT CARBOHYD 162 162
 FT CARBOHYD 207 207
 FT CARBOHYD 259 259
 FT CARBOHYD 299 299
 FT CARBOHYD 363 363
 FT CARBOHYD 386 386
 FT CARBOHYD 402 402
 FT CARBOHYD 413 413
 FT CARBOHYD 434 434
 FT CARBOHYD 438 438
 FT CARBOHYD 469 469
 FT CARBOHYD 474 474
 FT CARBOHYD 480 480
 FT CARBOHYD 490 490
 FT CARBOHYD 500 500
 FT CARBOHYD 514 514
 FT CARBOHYD 526 526
 FT CARBOHYD 535 535
 FT CARBOHYD 542 542
 FT CARBOHYD 550 550
 FT CARBOHYD 560 560
 FT CARBOHYD 567 567
 FT CARBOHYD 703 703
 FT CARBOHYD 771 771
 FT CARBOHYD 778 778
 FT CARBOHYD 794 794
 SQ SEQUENCE 990 AA; 114498 MW; 279B16BE55614F3 CRC64;

Query Match 48.5%; Score 48; DB 1; Length 990;
 Best Local Similarity 50.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RRWPPWWPKWPL 12
 ||:||| :||| :|||

Db 174 QEWPNWYWPL 185

RESULT 12.
 ENV_CAEVG STANDARD; PRT; 942 AA.

ID ENV_CAEVG
 AC P31627;
 DT 01-JUL-1993 (Rel. 26, created)
 DT 20-AUG-2001 (Rel. 40, last sequence update)
 DT 20-AUG-2001 (Rel. 40, last annotation update)
 DE ENV POLYPROTEIN PRECURSOR (COAT POLYPEPTIDE) [CONTAINS: SURFACE PROTEIN; TRANSMEMBRANE PROTEIN].
 GN ENV.
 OS Caprine arthritis encephalitis virus (strain G63) (CAEV).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TAXID=11662;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 81-95.
 RX MEDLINE=92015464; PubMed=1056067;
 RA Knowles D.P., Cheevers W.P., McGuire T.C., Brassfield A.L.,
 RA Harwood W.G., Stem T.A.;
 RT "Structure and genetic variability of envelope glycoproteins of two
 RT antigenic variants of caprine arthritis-encephalitis lentivirus.";
 RL J. Virol. 65:5744-5750(1991).

RP	REVISIONS.	
RA	Knowles D.P.;	[1]
RL	Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A.
CC		RX
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CC		RA
CC	EMBL; MG0855; AAB88709_2; -.	Harwood W.G., Stem T.A.;
DR	PIR; A41307; VCLJC6.	"Structure and genetic variability of envelope glycoproteins of two antigenic variants of caprine arthritis-encephalitis lentivirus.";
DR	InterPro; IPR000328; Env_GP41.	J. virol. 65:5744-5750(1991).
DR	Pfam; PF00517; GP41; 1.	[2]
FT	GLycoprotein; Coat protein; Polyprotein; Transmembrane.	SEQUENCE FROM N.A.
FT	PEPTIDE 1	RX
FT	CHAIN 81	Medline=91021037; PubMed=2171210;
FT	CHAIN 631	RX
FT	DOMAIN 1	Saltarelli M., Quezat G., Konings D.A., Vigne R., Clements J.E.;
FT	TRANSMEM 631	"Nucleotide sequence and transcriptional analysis of molecular clones of CAEV which generate infectious virus.";
FT	DOMAIN 660	RT
FT	TRANSMEM 799	RT
FT	DOMAIN 800	EMBL; M33677; AAA91829_1; -.
FT	TRANSMEM 942	DR
FT	CARBONYD 51	PIR; B41307; VCLJC6.
FT	CARBONYD 98	DR
FT	CARBONYD 131	InterPro; IPR000328; Env_GP41.
FT	CARBONYD 176	DR
FT	CARBONYD 226	Pfam; PF00517; GP41; 1.
FT	CARBONYD 328	CC
FT	CARBONYD 331	CC
FT	CARBONYD 348	CC
FT	CARBONYD 354	CC
FT	CARBONYD 370	CC
FT	CARBONYD 379	CC
FT	CARBONYD 400	CC
FT	CARBONYD 404	CC
FT	CARBONYD 435	CC
FT	CARBONYD 441	CC
FT	CARBONYD 447	CC
FT	CARBONYD 457	CC
FT	CARBONYD 467	CC
FT	CARBONYD 481	CC
FT	CARBONYD 493	CC
FT	CARBONYD 503	CC
FT	CARBONYD 509	CC
FT	CARBONYD 527	CC
FT	CARBONYD 534	CC
FT	CARBONYD 534	CC
SQ	SEQUENCE 942 AA;	SEQUENCE FROM N.A.
SQ	SEQUENCE 108437 MW;	RX
SQ	SEQUENCE 580E1F03D355F4A CRC64;	RA
Query Match	Score 47; DB 1; length 942;	RA
Best Local Similarity	60.0%; Pred. No. 35;	RA
Matches	6; Conservative	RA
OY	3 WPPWWPKWPL 12	Harwood W.G., Stem T.A.;
Db	;	"Structure and genetic variability of envelope glycoproteins of two antigenic variants of caprine arthritis-encephalitis lentivirus.";
Db	145 WPWNTYHWPL 154	J. virol. 65:5744-5750(1991).
RESULT	13	[2]
ENV_CAEVC	STANDARD; PRT; 966 AA.	SEQUENCE FROM N.A.
ID	ENV_CAEVC	RX
AC	P31626;	RA
DT	01-JUL-1993 (Rel. 26, Created)	RA
DT	01-JUL-1993 (Rel. 26, Last sequence update)	RT
DT	20-AUG-2001 (Rel. 40, Last annotation update)	RT
DE	ENV POLYPEPTIDE PRECURSOR (CoAT POLYPROTEIN) [CONTAINS: SURFACE PROTEIN; TRANSMEMBRANE PROTEIN].	RT
GN	Caprine arthrititis encephalitis virus (strain Cork) (CAEV).	RT
OS	Viruses; Retroviridae; Retroviridae; Lentivirus.	RT
OX	NCBI_TaxID:11661;	RT
Query Match	Score 47; DB 1; length 966;	RN
Best Local Similarity	60.0%; Pred. No. 36;	RN
Matches	6; Conservative	RN
OY	3 WPPWWPKWPL 12	[1]
Db	;	[2]
Db	145 WPWNTYHWPL 154	[2]
SEQUENCE	966 AA;	SEQUENCE FROM N.A.
SEQUENCE	110291 MW;	RX
SEQUENCE	2ADEB6A92BC1D69B CRC64;	RA
Query Match	Score 47; DB 1; length 966;	RA
Best Local Similarity	60.0%; Pred. No. 36;	RA
Matches	6; Conservative	RA
OY	3 WPPWWPKWPL 12	Harwood W.G., Stem T.A.;
Db	;	"Structure and genetic variability of envelope glycoproteins of two antigenic variants of caprine arthritis-encephalitis lentivirus.";
Db	145 WPWNTYHWPL 154	J. virol. 65:5744-5750(1991).
RESULT	13	[2]
ENV_CAEVC	STANDARD; PRT; 966 AA.	SEQUENCE FROM N.A.
ID	ENV_CAEVC	RX
AC	P31626;	RA
DT	01-JUL-1993 (Rel. 26, Created)	RA
DT	01-JUL-1993 (Rel. 26, Last sequence update)	RT
DT	20-AUG-2001 (Rel. 40, Last annotation update)	RT
DE	ENV POLYPEPTIDE PRECURSOR (CoAT POLYPROTEIN) [CONTAINS: SURFACE PROTEIN; TRANSMEMBRANE PROTEIN].	RT
GN	Caprine arthrititis encephalitis virus (strain Cork) (CAEV).	RT
OS	Viruses; Retroviridae; Retroviridae; Lentivirus.	RT
OX	NCBI_TaxID:11661;	RT

FT	CARBOHYD	387	387	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	403	403	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	414	414	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	435	435	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	439	439	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	470	470	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	475	475	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	481	481	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	491	491	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	501	501	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	515	515	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	527	527	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	537	537	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	542	542	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	543	543	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	568	568	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	697	697	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	755	755	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	772	772	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	788	788	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	822	822	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CONFLICT	900	900	R -> H (IN REF. 1; ARA49362).
SQ	SEQUENCE	983	AA;	113939 MN; E03BCC254EA78268 CRC64;

Query Match Similarity 47.5%; Score 47; DB 1; Length 983;
 Best Local Similarity 60.0%; Pred. No. 36; Mismatches 0;
 Matches 6; Conservative 1; Indels 0; Gaps 0;

QY 3 WPWWWWKWL 12
 ||| : |||
 Db 175 WPWNTYHWPL 184

Search completed: January 30, 2002, 11:52:22
 Job time: 201 sec